The crude oil thus obtained can subsequently be purified further, for example by removing suspended matter by treatment with polar solvents such as acetone or chloroform, followed by filtration or centrifugation. A further purification via chromatographic methods, distillation or crystallization is also possible.

To obtain the free fatty acids from the triglycerides, the latter are usually hydrolyzed as described above.

The invention furthermore relates to isolated nucleic acid sequences which encodes [sic] a polypeptide and which is [sic] composed of a combination of the nucleic acid sequences of a biosynthesis nucleic acid sequence of the fatty acid or lipid metabolism and one of the following nucleic acids:

a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 1,

b) nucleic acid sequences which are derived from the nucleic acid sequence shown in SEQ ID NO: 1 as the result of the degeneracy of the genetic code,

c) derivatives of the nucleic acid sequence shown in SEQ ID NO: 1 which encode polypeptides with the amino acid sequences shown in SEQ ID NO: 2 and which have at least 60% homology at the amino acid level,

d) a nucleic acid sequence with the sequence shown in SEQ ID NO: 3 or the amino-terminal portion of the coding region of this sequence.

These nucleic acid sequences according to the invention make possible the targeting of proteins in the method according to the invention.

Derivative(s) are to be understood as meaning, for example, functional homologs of the proteins encoded by SEQ ID NO: 1 or of their biological activity, that is to say proteins which [lacuna] the same biological reactions as those controlled by SEQ ID NO: 1. These genes also make possible an advantageous targeting of proteins. Biological activity is understood as meaning directing proteins, advantageously proteins which are involved in the fatty acid and/or lipid metabolism, within the cell.

The nucleic acid sequence(s) used in the method according to the invention (for the purposes of the application, the singular is to comprise the plural and vice versa) or fragments thereof can

which have been obtained by backtranslating a polypeptide sequence in accordance with the host-plant-specific codon usage are especially suitable.

Components of the nucleic acids according to the invention which may be mentioned are biosynthesis genes of the fatty acid and/or lipid metabolism such as advantageously a sequence which encodes proteins from among the following group of proteins:

Acyl-CoA dehydrogenase(s), Acyl-ACP [= acyl carrier protein] desaturase(s), Acyl-ACP thioesterase(s), fatty acid acyltransferase(s), fatty acid synthase(s), fatty acid hydroxylase(s), acetyl-coenzyme A carboxylase(s), acyl-coenzyme A oxidase(s), fatty acid desaturase(s), fatty acid acetylenases, lipoxygenases, triacylglycerol lipases, allenoxide synthases, hydroperoxide lyases and/or fatty acid elongase(s). They are preferably nucleic acids which encode one of the following proteins: fatty acid acyltransferase(s), Δ4 desaturase, Δ5 desaturase, Δ6 desaturase, Δ9 desaturase, Δ12 desaturase, Δ15 desaturase and/or a fatty acid elongase.

The nucleic acid sequences mentioned encode encode [sic] what are known as fusion proteins, component of the fusion protein being a polypeptide with the sequence mentioned in SEQ ID NO: 2 or a functionally equivalent part thereof. The second moiety of the fusion protein can be, for example, a further polypeptide with enzymatic activity, such as, for example, the abovementioned proteins.

In the method according to the invention, the nucleic acids can be combined advantageously with further genes of fatty acid biosynthesis. Examples of such genes are the acetyltransferases, further desaturases or elongases of unsaturated or saturated fatty acids as described in WO 00/12720. The combination with, for example, NADH cytochrome B5 reductases, which are capable of accepting or donating reduction equivalents, is advantageous for the in vivo and, specifically, the in vitro synthesis.

The proteins used in the method according to the invention are understood as meaning proteins which comprise an amino acid sequence shown in sequence SEQ ID NO: 2 or a sequence obtainable therefrom by substitution, inversion, insertion or deletion of one or more amino acid residues, the biological activity of the protein shown in SEQ ID NO: 2 being retained or not being reduced substantially. The term "not reduced substantially" is understood as meaning all those proteins which retain at least 10%, preferably 20%, especially preferably 30%, of the biological